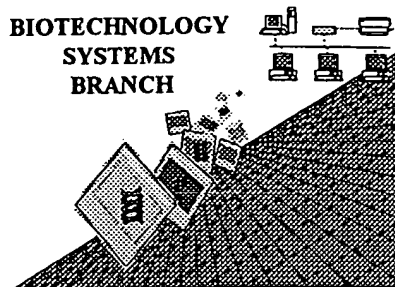


0106

02CJ

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

# CRF Diskette Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following CRF diskette:

Application Serial Number:

09/439,311

Filing Date:

11/12/99

Classification:

Date Processed by STIC:

11/30/99

Point-of-Contact/Telephone No.: Mark Spencer 703 - 308 - 4212

## Nature of Problem:

The diskette was:

- ☐ Damaged
- ☐ Unreadable
- ☐ Blank (no files present on diskette)
- ☐ Contained an empty file (filename present, but no bytes in file)
- ☐ A computer virus was detected on the diskette. The STIC will not process the diskette through the Data Capture System.

Name of virus: \_\_\_\_\_

- ☐ The Sequence Listing was not saved in ASCII (DOS) text.

- ☒ The diskette contained an error that disrupted normal processing:

Sequence Listing was embedded in one of  
the disk files submitted (see attached).

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/439,311

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                         (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                         (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                         This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)      (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

09/439,311

Filename: 78560p ~1.doc

carrier vaccines such as *Salmonella* or *Shigella* attenuated, live vaccines, for use as a bivalent vaccine.

see next page

09/439,371

SEQUENCE LISTING

□

□  
5 <110> Guerry, Patricia  
□

(partial listing)

Sequence Listing began on p. 32 of one of the  
three files submitted on diskette. Per 1.824(a)(1)  
of Sequence Rules, "The computer readable form shall  
contain a single 'Sequence Listing'..." Please submit  
Sequence Listing only — do not include any other  
information. Also, do not include disk files other  
than Sequence Listing.

FSI

Please review the  
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
<223> fields of each sequence which presents at least one n or Xaa.

Also,  
Please see item 5 on Ena summary sheet.